SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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 (A) NAME: Federal Republic of Germany, ulti-
                        mately represented by the Director
                        of the Robert-Koch-Institut
 (B) STREET: Nordufer 20
 (C) CITY: Berlin
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 (D) STATE OR
     PROVINCE: Berlin
 (E) COUNTRY: Germany
 (F) POSTAL CODE: 13353

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 (ii) TITLE OF INVENTION: Costimulating polypeptide of T cells,
monoclonal antibodies, and the preparation and use thereof

 (iii) NUMBER OF SEQUENCES: 4

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 (iv) COMPUTER-READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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 (v) CURRENT APPLICATION DATA:
      APPLICATION NUMBER:

(2) INFORMATION FOR SEQ ID NO: 1:

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 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2641 base pairs
 (B) TYPE: Nucleotides
 (C) STRANDEDNESS: Double
35
 (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: cDNA

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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CGAGAGCCTG AATTCACTGT CAGCTTTGAA CACTGAACGC GAGGACTGTT AAGTGTTTCT     60

GGCAAACATG AAGTCAGGCC TCTGGTATTT CTTTCTCTTC TGCTTGCGCA TTAAAGTTTT    120

AACAGGAGAA ATCAATGGTT CTGCCAATTA TGAGATGTTT ATATTTCACA ACGGAGGTGT    180

ACAAATTTTA TGCAAATATC CTGACATTGT CCAGCAATTT AAAATGCAGT TGCTGAAAGG    240

GGGGCAAATA CTCTGCGATC TCACTAAGAC AAAAGGAAGT GGAAACACAG TGTCCATTAA    300

GAGTCTGAAA TTCTGCCATT CTCAGTTATC CAACAACAGT GTCTCTTTTT TTCTATACAA    360

CTTGGACCAT TCTCATGCCA ACTATTACTT CTGCAACCTA TCAATTTTTG ATCCTCCTCC    420

TTTTAAAGTA ACTCTTACAG GAGGATATTT GCATATTTAT GAATCACAAC TTTGTTGCCA    480

GCTGAAGTTC TGGTTACCCA TAGGATGTGC AGCCTTTGTT GTAGTCTGCA TTTTGGGATG    540

CATACTTATT TGTTGGCTTA CAAAAAAGAA GTATTCATCC AGTGTGCACG ACCCTAACGG    600
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TGAATACATG TTCATGAGAG CAGTGAACAC AGCCAAAAAA TCTAGACTCA CAGATGTGAC    660

CCTATAATAT GGAACTCTGG CACCCAGGCA TGAAGCACGT TGGCCAGTTT TCCTCAACTT    720

GAAGTGCAAG ATTCTCTTAT TTCCGGGACC ACGGAGAGTC TGACTTAACT ACATACATCT    780

TCTGCTGGTG TTTTGTTCAA TCTGGAAGAA TGACTGTATC AGTCAATGGG GATTTTAACA    840

GACTGCCTTG GTACTGCCGA GTCCTCTCAA AACAAACACC CTCTTGCAAC CAGCTTTGGA    900

GAAAGCCCAG CTCCTGTGTG CTCACTGGGA GTGGAATCCC TGTCTCCACA TCTGCTCCTA    960

GCAGTGCATC AGCCAGTAAA ACAAACACAT TTACAAGAAA AATGTTTTAA AGATGCCAGG   1020

GGTACTGAAT CTGCAAAGCA AATGAGCAGC CAAGGACCAG CATCTGTCCG CATTTCACTA   1080

TCATACTACC TCTTCTTTCT GTAGGGATGA GAATTCCTCT TTTAATCAGT CAAGGGAGAT   1140

GCTTCAAAGC TGGAGCTATT TTATTTCTGA GATGTTGATG TGAACTGTAC ATTAGTACAT   1200

ACTCAGTACT CTCCTTCAAT TGCTGAACCC CAGTTGACCA TTTTACCAAG ACTTTAGATG   1260

CTTTCTTGTG CCCTCAATTT TCTTTTTAAA AATACTTCTA CATGACTGCT TGACAGCCCA   1320

ACAGCCACTC TCAATAGAGA GCTATGTCTT ACATTCTTTC CTCTGCTGCT CAATAGTTTT   1380

ATATATCTAT GCATACATAT ATACACACAT ATGTATATAA AATTCATAAT GAATATATTT   1440

GCCTATATTC TCCCTACAAG AATATTTTTG CTCCAGAAAG ACATGTTCTT TTCTCAAATT   1500

CAGTTAAAAT GGTTTACTTT GTTCAAGTTA GTGGTAGCAA ACATTGCCCG GAATTGAAAG   1560

CAAATTTATT TTATTATCCT ATTTTCTACC ATTATCTATG TTTTCATGGT GCTATTAATT   1620

ACAAGTTTAG TTCTTTTTGT AGATCATATT AAAATTGCAA ACAAAATCAT CTTTAATGGG   1680

CCAGCATTCT CATGGGGTAG AGCAGAATAT TCATTTAGCC TGAAGCTGC AGTTACTATA    1740

GGTTGCTGTC AGACTATACC CATGGTGCCT CTGGGCTTGA CAGGTCAAAA TGGTCCCCAT   1800

CAGCCTGGAG CAGCCCTCCA GACCTGGGTG GAATTCCAGG GTTGAGAGAC TCCCCTGAGC   1860

CAGAGGCCAC TAGGTATTCT TGCTCCCAGA GGCTGAAGTC ACCCTGGGAA TCACAGTGGT   1920

CTACCTGCAT TCATAATTCC AGGATCTGTG AAGAGCACAT ATGTGTCAGG GCACAATTCC   1980

CTCTCATAAA AACCACACAG CCTGGAAATT GGCCCTGGCC CTTCAAGATA GCCTTCTTTA   2040

GAATATGATT TGGCTAGAAA GATTCTTAAA TATGTGGAAT ATGATTATTC TTAGCTGCAA   2100

TATTTCTCT ACTTCCTGTC TGCATGCCCA AGGCTTCTGA AGCAGCCAAT GTCGATGCAA    2160

CAACATTTGT AACTTTAGGT AAACTGGGAT TATGTTGTAG TTTAACATTT TGTAACTGTG   2220

TGCTTATAGT TTACAAGTGA GACCCGATAT GTCATTATGC ATACTTATAT TATCTTAAGC   2280

ATGTGTAATG CTGGATGTGT ACAGTACAGT ACTGAACTTG TAATTTGAAT CTAGTATGGT   2340

GTTCTGTTTT CAGCTGACTT GGACAACCTG ACTGGCTTTG CACAGGTGTT CCCTGAGTTG   2400

TTTGCAGGTT TCTGTGTGTG GGGTGGGGTA TGGGGAGGAG AACCTTCATG GTGGCCCACC   2460

TGGCCTGGTT GTCCAAGCTG TGCCTCGACA CATCCTCATC CCCAGCATGG GACACCTCAA   2520
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GATGAATAAT AATTCACAAA ATTTCTGTGA AATCAAATCC AGTTTTAAGA GGAGCCACTT    2580

ATCAAAGAGA TTTTAACAGT AGTAAGAAGG CAAAGAATAA ACATTTGATA TTCAGCAACT    2640

G                                                                     2641
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(2) INFORMATION FOR SEQ ID NO: 2:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 199 amino acids
        (B) TYPE: Amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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Met Lys Ser Gly Leu Trp Tyr Phe Phe Leu Phe Cys Leu Arg Ile Lys
1               5               10              15

Val Leu Thr Gly Glu Ile Asn Gly Ser Ala Asn Tyr Glu Met Phe Ile
            20              25              30

Phe His Asn Gly Gly Val Gln Ile Leu Cys Lys Tyr Pro Asp Ile Val
        35              40              45

Gln Gln Phe Lys Met Gln Leu Leu Lys Gly Gly Gln Ile Leu Cys Asp
    50              55              60

Leu Thr Lys Thr Lys Gly Ser Gly Asn Thr Val Ser Ile Lys Ser Leu
65              70              75              80

Lys Phe Cys His Ser Gln Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
            85              90              95

Tyr Asn Leu Asp His Ser His Ala Asn Tyr Tyr Phe Cys Asn Leu Ser
            100             105             110

Ile Phe Asp Pro Pro Pro Phe Lys Val Thr Leu Thr Gly Gly Tyr Leu
        115             120             125

His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Phe Trp Leu Pro
    130             135             140

Ile Gly Cys Ala Ala Phe Val Val Val Cys Ile Leu Gly Cys Ile Leu
145             150             155             160

Ile Cys Trp Leu Thr Lys Lys Lys Tyr Ser Ser Ser Val His Asp Pro
            165             170             175

Asn Gly Glu Tyr Met Phe Met Arg Ala Val Asn Thr Ala Lys Lys Ser
            180             185             190

Arg Leu Thr Asp Val Thr Leu
        195
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(2) INFORMATION FOR SEQ ID NO: 3:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
5   (B) TYPE: Nucleotides
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: DNA
  (iii) HYPOTHETICAL: Yes
10   (iv) ANTISENSE: NO

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
MGNCTSACNG AYGTNAC   17

15 (2) INFORMATION FOR SEQ ID NO: 4:

    (i)   SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17 base pairs
        (B) TYPE: Nucleotides
20   (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
   (ii) MOLECULE TYPE: DNA
  (iii) HYPOTHETICAL: Yes
   (iv) ANTISENSE: NO
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    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
MGNYTDACNG AYGTNAC   17